

RAW SEQUENCE LISTING

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Application Serial Number: 10/541,427
Source: PU/10
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RAW SEQUENCE LISTING

DATE: 11/07/2005

PATENT APPLICATION: US/10/541,427

TIME: 09:31:22

Input Set : A:\Sequence List.txt

Output Set: N:\CRF4\11072005\J541427.raw

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3 <110> APPLICANT: Zelinski, Thomas
4     Kessler, Maria
5     Hauer, Bernhard
7 <120> TITLE OF INVENTION: METHODS FOR PRESERVING AND/OR STORING CELLS HAVING A NITRILASE
8     OR NITRILE HYDRATASE AVTIVITY
10 <130> FILE REFERENCE: 12810-00105-US
-> 12 <140> CURRENT APPLICATION NUMBER: US/10/541,427
-> 12 <141> CURRENT FILING DATE: 2005-07-05
12 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/014880
13 <151> PRIOR FILING DATE: 2003-12-24
15 <150> PRIOR APPLICATION NUMBER: DE 103 00 500.5
16 <151> PRIOR FILING DATE: 2003-01-08
18 <160> NUMBER OF SEQ ID NOS: 2
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1071
24 <212> TYPE: DNA
25 <213> ORGANISM: Alcaligenes faecalis
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(1068)
30 <223> OTHER INFORMATION: coding for nitrilase
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33 atg cag aca aga aaa atc gtc cgg gca gcc gcc gta cag gcc gcc tct      48
34 Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser
35   1             5             10             15
36 ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct      96
37 Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
38   20             25             30
39 cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc     144
40 Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
41   35             40             45
42 tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg     192
43 Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
44   50             55             60
45 tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac     240
46 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
47  65             70             75             80
48 agt gca gag ttt caa cgc att gcc cag gcc gca cgg acc ttg ggt att     288
49 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
50   85             90             95
51 ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg     336
52 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu

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53		100		105		110		
54	ggc caa tgc	ctg atc gac gac	aag ggc gag	atg ctg tgg	tcg cgt cgc	384		
55	Gly Gln Cys	Leu Ile Asp Asp	Lys Gly Glu	Met Leu Trp	Ser Arg Arg			
56		115		120		125		
57	aaa ctc aaa	ccc acg cat gta	gag cgc acc gta	ttt ggt gaa	ggg tat	432		
58	Lys Leu Lys	Pro Thr His Val	Glu Arg Thr Val	Phe Gly Glu	Gly Tyr			
59		130		135		140		
60	gcc cgt gat	ctg att gtg tcc	gac aca gaa	ctg gga cgc	gtc ggt gct	480		
61	Ala Arg Asp	Leu Ile Val Ser	Asp Thr Glu	Leu Gly Arg	Val Gly Ala			
62	145		150		155		160	
63	cta tgc tgc	tgg gag cat ttg	tcg ccc ttg	agc aag tac	gcg ctg tac	528		
64	Leu Cys Cys	Trp Glu His Leu	Ser Pro Leu	Ser Lys Tyr	Ala Leu Tyr			
65		165		170		175		
66	tcc cag cat	gaa gcc att cac	att gct gcc	tgg ccg tcg	ttt tcg cta	576		
67	Ser Gln His	Glu Ala Ile His	Ile Ala Ala	Trp Pro Ser	Phe Ser Leu			
68		180		185		190		
69	tac agc gaa	cag gcc cac gcc	ctc agt gcc	aag gtg aac	atg gct gcc	624		
70	Tyr Ser Glu	Gln Ala His Ala	Leu Ser Ala	Lys Val Asn	Met Ala Ala			
71		195		200		205		
72	tcg caa atc	tat tcg gtt gaa	ggc cag tgc	ttt acc atc	gcc gcc agc	672		
73	Ser Gln Ile	Tyr Ser Val Glu	Gly Gln Cys	Phe Thr Ile	Ala Ala Ser			
74		210		215		220		
75	agt gtg gtc	acc caa gag acg	cta gac atg	ctg gaa gtg	ggg gaa cac	720		
76	Ser Val Val	Thr Gln Glu Thr	Leu Asp Met	Leu Glu Val	Gly Glu His			
77	225		230		235		240	
78	aac gcc ccc	ttg ctg aaa gtg	ggc ggc ggc	agt tcc atg	att ttt gcg	768		
79	Asn Ala Pro	Leu Leu Lys Val	Gly Gly Gly	Ser Ser Met	Ile Phe Ala			
80		245		250		255		
81	ccg gac gga	cgc aca ctg gct	ccc tac ctg	cct cac gat	gcc gag ggc	816		
82	Pro Asp Gly	Arg Thr Leu Ala	Pro Tyr Leu	Pro His Asp	Ala Glu Gly			
83		260		265		270		
84	ttg atc att	gcc gat ctg aat	atg gag gag	att gcc ttc	gcc aaa gcg	864		
85	Leu Ile Ile	Ala Asp Leu Asn	Met Glu Glu	Ile Ala Phe	Ala Lys Ala			
86		275		280		285		
87	atc aat gac	ccc gta ggc cac	tat tcc aaa	ccc gag gcc	acc cgt ctg	912		
88	Ile Asn Asp	Pro Val Gly His	Tyr Ser Lys	Pro Glu Ala	Thr Arg Leu			
89		290		295		300		
90	gtg ctg gac	ttg ggg cac cga	gac ccc atg	act cgg gtg	cac tcc aaa	960		
91	Val Leu Asp	Leu Gly His Arg	Asp Pro Met	Thr Arg Val	His Ser Lys			
92	305		310		315		320	
93	agc gtg acc	agg gaa gag gct	ccc gag caa	ggg gtg caa	agc aag att	1008		
94	Ser Val Thr	Arg Glu Glu Ala	Pro Glu Gln	Gly Val Gln	Ser Lys Ile			
95		325		330		335		
96	gcc tca gtc	gct atc agc cat	cca cag gac	tcg gac aca	ctg cta gtg	1056		
97	Ala Ser Val	Ala Ile Ser His	Pro Gln Asp	Ser Asp Thr	Leu Leu Val			
98		340		345		350		
99	caa gag ccg	tct tga				1071		
100	Gln Glu Pro	Ser						
101		355						

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103 <210> SEQ ID NO: 2

104 <211> LENGTH: 356

105 <212> TYPE: PRT

106 <213> ORGANISM: *Alcaligenes faecalis*

108 <400> SEQUENCE: 2

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109 Met Gln Thr Arg Lys Ile Val Arg Ala Ala Val Gln Ala Ala Ser
110   1           5           10           15
111 Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
112           20           25           30
113 Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
114           35           40           45
115 Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
116           50           55           60
117 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
118           65           70           75           80
119 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
120           85           90           95
121 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
122           100          105          110
123 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
124           115          120          125
125 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
126           130          135          140
127 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
128           145          150          155          160
129 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
130           165          170          175
131 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
132           180          185          190
133 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
134           195          200          205
135 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
136           210          215          220
137 Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His
138           225          230          235          240
139 Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala
140           245          250          255
141 Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly
142           260          265          270
143 Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala
144           275          280          285
145 Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu
146           290          295          300
147 Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys
148           305          310          315          320
149 Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile
150           325          330          335
151 Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val
152           340          345          350

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153 Gln Glu Pro Ser

154 355

VERIFICATION SUMMARY

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12 M:270 C: Current Application Number differs, Replaced Current Application No

12 M:271 C: Current Filing Date differs, Replaced Current Filing Date